

Figure 1/1
SEQ ID No.: 1

DNA sequence:

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1  ATGAGGGGGCT CGCATCACCA TCACCATCAC GCTGCTGACG ATGACGATAA
51  AATGAGGGGCG ATGCTACCGC TATTTGAGCC CAAGGGCCGG GTCCTCCTGG
101 TCGACGGCCA CCACCTGGCC TACCGCACCT TCCAAGCCCT GAAGGGCCCTC
151 ACCACCAGCC GGGGGGAGCC GGTGCAGGCG GTCTACGGCT TCGCCAAGAG
201 CCTCCTCAAG GCCCTCAAGG AGGACGGGGA CGCGGTGATC GTGGTCTTTG
251 ACGCCAAGGC CCCCTCCTTC CGCCACGAGG CCTACGGGGG GTACAAGGCG
301 GGCCGGGCCC CCACGCCGGA GGACTTTCCC CGGCAACTCG CCCTCATCAA
351 GGAGCTGGTG GACCTCCTGG GGCTGGCGCG CCTCGAGGTC CCGGGCTACG
401 AGGCGGACGA CGTCCTGGCC AGCCTGGCCA AGAAGGCGGA AAAGGAGGGC
451 TACGAGGTCC GCATCCTCAC CGCCGACAAA GACCTTTACC AGCTCCTTTC
501 CGACCGCATC CACGTCCTCC ACCCCGAGGG GTACCTCATC ACCCCGGCCT
551 GGCTTTGGGA AAAGTACGGC CTGAGGCCCG ACCAGTGGGC CGACTACCGG
601 GCCCTGACCG GGGACGAGTC CGACAACCTT CCCGGGGTCA AGGGCATCGG
651 GGAGAAGACG GCGAGGAAGC TTCTGGAGGA GTGGGGGAGC CTGGAAGCCC
701 TCCTCAAGAA CCTGGACCGG CTGAAGCCCG CCATCCGGGA GAAGATCCTG
751 GCCACATGG ACGATCTGAA GCTCTCCTGG GACCTGGCCA AGGTGCGCAC
801 CGACCTGCCC CTGGAGGTGG ACTTCGCCAA AAGGCGGGAG CCCGACCGGG
851 AGAGGCTTAG GGCCTTTCTG GAGAGGCTTG AGTTTGGCAG CCTCCTCCAC
901 GAGTTCGGCC TTCTGGAAAG CCCCTATGAC AACTACGTCA CCATCCTTGA
951 TGAAGAAACA CTGAAAGCGT GGATTGCGAA GCTGGAAAAA GCGCCGGTAT
1001 TTGCATTTGA TACCGAAACC GACAGCCTTG ATAACATCTC TGCTAACCTG
1051 GTCGGGCTTT CTTTTGCTAT CGAGCCAGGC GTAGCGGCAT ATATTCCGGT
1101 TGCTCATGAT TATCTTGATG CGCCCGATCA AATCTCTCGC GAGCGTGCAC
1151 TCGAGTTGCT AAAACCGCTG CTGGAAGATG AAAAGGCGCT GAAGGTCGGG
1201 CAAAACCTGA AATACGATCG CGGTATTCTG GCGAACTACG GCATTGAACT
1251 GCGTGGGATT GCGTTTGATA CCATGCTGGA GTCCTACATT CTCAATAGCG
1301 TTGCCGGGCG TCACGATATG GACAGCCTCG CGGAACGTTG GTTGAAGCAC
1351 AAAACCATCA CTTTTGAAGA GATTGCTGGT AAAGGCAAAA ATCAACTGAC
1401 CTTTAACAG ATTGCCCTCG AAGAAGCCGG ACGTTACGCC GCCGAAGATG
1451 CAGATGTCAC CTTGCAGTTG CATCTGAAAA TGTGGCCGGA TCTGCAAAAA
1501 CACGAGAGGC TCCTTTGGCT TTACCGGGAG GTGGAGAGGC CCCTTTCCGC
1551 TGTCTGGGCC CACATGGAGG CCACGGGGGT GCGCCTGGAC GTGGCCTATC
1601 TCAGGGCCTT GTCCCTGGAG GTGGCCGAGG AGGTCGCCCC CCTCGAGGCC
1651 GAGGTCTTCC GCCTGGCCGG CCACCCCTTC AACCTCAACT CCCGGGACCA
1701 GCTGGAAAGG GTCCTCTTTG ACGAGCTAGG GCTTCCCGCC ATCGGCAAGA
1751 CGGAGAAGAC CGGCAAGCGC TCCACCAGCG CCGCCGTCCT GGAGGCCCTC
1801 CGCGAGGCC ACCCATCGT GGAGAAGATC CTGCAGTACC GGGAGCTCAC
1851 CAAGCTGAAG AGCACCTACA TTGACCCCTT GCCGGACCTC ATCCACCCCA
1901 GGACGGGCCG CCTCCACACC CGCTTCAACC AGACGGCCAC GGCCACGGGC
1951 AGGCTAAGTA GCTCCGATCC CAACCTCCAG AACATCCCCG TCCGCACCCC
2001 GCTTGGGCAG AGGATCCGCC GGGCCTTCAT CGCCGAGGAG GGGTGGCTAT
2051 TGGTGGCCCT GGAATATAGC CAGATAGAGC TCAGGGTGCT GGCCACCTC
2101 TCCGGCGACG AGAACCTGAT CCGGGTCTTC CAGGAGGGGC GGGACATCCA
2151 CACGGAGACC GCCAGCTGGA TGTTGCGCGT CCCCCGGGAG GCCGTGGACC
2201 CCCTGATGCG CCGGGCGGCC AAGACCATCA ACTTCGGGGT CCTCTACGGC
2251 ATGTCGGCCC ACCGCCTCTC CCAGGAGCTA GCCATCCCTT ACGAGGAGGC
2301 CCAGGCCTTC ATTGAGCGCT ACTTTCAGAG CTTCCCCAAG GTGCGGGCCT
2351 GGATTGAGAA GACCCTGGAG GAGGGCAGGA GGCGGGGGTA CGTGGAGACC
2401 CTCTTCGGCC GCCGCCGCTA CGTGCCAGAC CTAGAGGCCC GGGTGAAGAG
2451 CGTGCGGGAG GCGGCCGAGC GCATGGCCTT CAACATGCCC GTCCAGGGCA
2501 CCGCCGCCGA CCTCATGAAG CTGGCTATGG TGAAGCTCTT CCCCAGGCTG

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Figure 1/2
SEQ ID No.: 1

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2551 GAGGAAATGG GGGCCAGGAT GCTCCTTCAG GTCCACGACG AGCTGGTCCT
2601 CGAGGCCCCA AAAGAGAGGG CGGAGGCCGT GGCCCGGCTG GCCAAGGAGG
2651 TCATGGAGGG GGTGTATCCC CTGGCCGTGC CCCTGGAGGT GGAGGTGGGG
2701 ATAGGGGAGG ACTGGCTCTC CGCCAAGGAG TGA

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SEQ ID No.: 7

amino acid sequence:

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1  MRGSHHHHHH AADDDDKMRG MLPLFEPKGR VLLVDGHHLA YRTFHALKGL
51  TTSRGEPVQA VYGFAKSLLK ALKEDGDAVI VVFDKAPSF RHEAYGGYKA
101 GRAPTPEDFP RQLALIKELV DLLGLARLEV PGYEADDVLA SLAKKAEKEG
151 YEVRILTADK DLYQLLSDRI HVLHPEGYLI TPRAWLEKYG LRPDQWADYR
201 ALTGDESDNL PGVKGIGECT ARKLLEEWGS LEALLKNLDR LKPAIREKIL
251 AHMDDLKLSW DLAKVRTDLP LEVDFAKRRE PDRERLRAFL ERLEFGSLH
301 EFGLLESPYD NYVTILDEET LKAWIAKLEK APVFAFDTET DSLDNISANL
351 VGLSFAIEPG VAAYIPVAHD YLDAPDQISR ERALELLKPL LEDEKALKVG
401 QNLKYDRGIL ANYGIELRGI AFDTMLESYI LNSVAGRHDM DSLAERWLKH
451 KTITFEEIAG KGKNQLTFNQ IALEEAGRYA AEDADVTLOL HLKMWPDLQK
501 HERLLWLYRE VERPLSAVLA HMEATGVRLD VAYLRALSLE VAEVARLEA
551 EVFRLAGHPF NLNSRDQLER VLFDELGLPA IGKTEKTGKR STSAÄVLEAL
601 REAHPIVEKI LQYRELTKLK STYIDPLPDL IHPRTGRLHT RFNQATATATG
651 RLSSSDPNLQ NIPVRTPLGQ RIRRAFIAEE GWLLVALDYS QIELRVLAHL
701 SGDENLIRVF QEGRDIHTET ASWMFGVPRE AVDPLMRRAA KTINFGVLYG
751 MSAHRLSQEL AIPYEEAQAF IERYFQSFPK VRAWIEKTLE EGRRRGYVET
801 LFGRRRYVPD LEARVKSVRE AAERMAFNMP VQGTADLMK LAMVKLFPRL
851 EEMGARMLLQ VHDELVLLEAP KERAFAVARL AKEVMEGVYP LAVPLEVEVG
901 IGEDWLSAKE

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Figure 2/1
SEQ ID No.: 2

DNA sequence:

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1  ATGAGGGGCT CGCATCACCA TCACCATCAC GCTGCTGACG ATGACGATAA
51  AATGAGGGGC ATGCTACCGC TATTTGAGCC CAAGGGCCGG GTCCTCCTGG
101 TCGACGGCCA CCACCTGGCC TACCGCACCT TCCACGCCCT GAAGGGCCTC
151 ACCACCAGCC GGGGGGAGCC GGTGCAGGCG GTCTACGGCT TCGCCAAGAG
201 CCTCCTCAAG GCCCTCAAGG AGGACGGGGA CGCGGTGATC GTGGTCTTTG
251 ACGCCAAGGC CCCCTCCTTC CGCCACGAGG CCTACGGGGG GTACAAGGCG
301 GGCCGGGCCC CCACGCCGGA GGACTTTCCC CGGCAACTCG CCCTCATCAA
351 GGAGCTGGTG GACCTCCTGG GGCTGGCGCG CCTCGAGGTC CCGGGCTACG
401 AGGCGGACGA CGTCTGGGCC AGCCTGGCCA AGAAGGCGGA AAAGGAGGCG
451 TACGAGGTCC GCATCCTCAC CGCCGACAAA GACCTTTACC AGTCTCTTTC
501 CGACCGCATC CACGTCTCTC ACCCCGAGGG GTACCTCATC ACCCCGGCCT
551 GGCTTTGGGA AAAGTACGGC CTGAGGCCCC ACCAGTGGGC CGACTACCGG
601 GCCCTGACCG GGGACGAGTC CGACAACCTT CCCGGGGTCA AGGGCATCGG
651 GGAGAAGACG GCGAGGAAGC TTCTGGAGGA GTGGGGGAGC CTGGAAGCCC
701 TCCTCAAGAA CCTGGACCGG CTGAAGCCCC CCATCCGGGA GAAGATCCTG
751 GCCCACATGG ACGATCTGAA GCTCTCCTGG GACCTGGCCA AGGTGCGCAC
801 CGACCTGCCC CTGGAGGTGG ACTTCGCCAA AAGGCGGGAG CCCGACGGGG
851 AGAGGCTTAG GGCCTTTCTG GAGAGGCTTG AGTTTGGCAG CCTCCTCCAC
901 GAGTTCGGCC TTCTGGAAGC CCCCTATGAC AACTACGTCA CCATCCTTGA
951 TGAAGAAACA CTGAAAGCGT GGATTGCGAA GCTGGAAAAA GCGCCGGTAT
1001 TTGCATTTGA TACCGAAACC GACAGCCTTG ATAACATCTC TGCTAACCTG
1051 GTCGGGCTTT CTTTGTGCTAT CGAGCCAGGC GTAGCGGCAT ATATTCCGGT
1101 TGCTCATGAT TATCTTGATG CGCCCGATCA AATCTCTCGC GAGCGTGCAC
1151 TCGAGTTGCT AAAACCGCTG CTGGAAGATG AAAAGGCGCT GAAGGTCGGG
1201 CAAAACCTGA AATACGATCG CGGTATTCTG GCGAACTACG GCATTGAACT
1251 GCGTGGGATT GCGTTTGATA CCATGCTGGA GTCCTACATT CTCAATAGCG
1301 TTGCCGGGCG TCACGATATG GACAGCCTCG CGGAACGTTG GTTGAAGCAC
1351 AAAACCATCA CTTTTGAAGA GATTGCTGGT AAAGGCAAAA ATCAACTGAC
1401 CTTTAAQAG ATTGCCCTCG AAGAAGCCGG ACGTTACGCC GCCGAAGATG
1451 CAGATGTQAC CTTGCAGTTG CATCTGAAAA TGTGGCCGGA TCTGCAAAAA
1501 CACAAAGGSC CGTTGAACGT CTTGAGAAAT ATCGAAATGC CGCTGGTGCC
1551 GGTGCTTTCA CGCATTGAAC GTAACGGTGT GCGCCTGGAC GTGGCCTATC
1601 TCAGGGCCTT GTCCTTGAGG GTGGCCGAGG AGATCGCCCG CCTCGAGGCC
1651 GAGGTCTTCC GCCTGGCCGG CCACCCCTTC AACCTCAACT CCCGGGACCA
1701 GCTGGAAAGG GTCCTCTTTG ACGAGCTAGG GCTTCCCGCC ATCGGCAAGA
1751 CGGAGAAGAC CGGCAAGCGC TCCACCAGCG CCGCCGTCCT GGAGGCCCTC
1801 CGCGAGGCCC ACCCATCGT GGAGAAGATC CTGCAGTACC GGGAGCTCAC
1851 CAAGCTGAAG AGCACCTACA TTGACCCCTT GCCGGACCTC ATCCACCCCA
1901 GGACGGGCCG CCTCCACACC CGCTTCAACC AGACGGCCAC GGCCACGGGC
1951 AGGCTAAGTA GTCCTGATCC CAACCTCCAG AACATCCCCG TCCGCACCCC
2001 GCTTGGGCAG AGGATCCGCC GGGCCTTCAT CGCCGAGGAG GGGTGGCTAT
2051 TGGTGGCCCT GGAATATAGC CAGATAGAGC TCAGGGTGCT GGCCACCTC
2101 TCCGGCGACG AGAACCTGAT CCGGTCTTTC CAGGAGGGGC GGGACATCCA
2151 CACGGAGACC GCCAGCTGGA TGTTGCGCGT CCCCCGGGAG GCCGTGGACC
2201 CCCTGATGCG CCGGGCGGCC AAGACCATCA ACTTCGGGGT CCTCTACGGC
2251 ATGTCGGCCC ACCGCCTCTC CCAGGAGCTA GCCATCCCTT ACGAGGAGGC
2301 CCAGGCCTTC ATTGAGCGCT ACTTTCAGAG CTTCCTCAAG GTGCGGGCCT
2351 GGATTGAGAA GACCCTGGAG GAGGGCAGGA GGCGGGGGTA CGTGGAGACC
2401 CTCTTCGGCC GCCGCCGCTA CGTGCCAGAC CTAGAGGCCC GGGTGAAGAG
2451 CGTGCGGGAG GCGGCCGAGC GCATGGCCTT CAACATGCCC GTCCAGGGCA
2501 CCGCCGCCGA CCTCATGAAG CTGGCTATGG TGAAGCTCTT CCCCAGGCTG

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Figure 2/2
SEQ ID No.: 2

2551 GAGGAAATGG GGGCCAGGAT GCTCCTTCAG GTCCACGACG AGCTGGTCCCT
2601 CGAGGCCCCA AAAGAGAGGG CGGAGGCCGT GGCCCGGCTG GCCAAGGAGG
2651 TCATGGAGGG GGTGTATCCC CTGGCCGTGC CCCTGGAGGT GGAGGTGGGG
2701 ATAGGGGAGG ACTGGCTCTC CGCCAAGGAG TGA

SEQ ID No.: 8

amino acid sequence:

1 MRGSHHHHHH AADDDDKMRG MLPLFEPKGR VLLVDGHHLA YRTFHALKGL
51 TTSRGEPVQA VYGFAXSLK ALKEDGDAVI VVFDKAPSF RHEAYGGYKA
101 GRAPTPEDFP RQLALIKELV DLLGLARLEV PGYEADDVLA SLAKKAEKEG
151 YEVRIITADK DLYQLLSORI HVLHPEGYLI TPAWLWEKYG LRPDQWADYR
201 ALTGDESDNL PGVKGIGKKT ARKLLEEWGS LEALLKNLDR LKPAIREKIL
251 AHMDDLKLSW DLAKVRTDLP LEVDFAKRRE PDRERLRAFL ERLEFGSLLH
301 EFGLLESFYD NYVTILDEET LKAWIAKLEK APVFADFDTET DSLDNISANL
351 VGLSFAIEPG VAAYIPVAHD YLDAPDQISR ERALELLKPL LEDEKALKVG
401 QNLKYDRGIL ANYGIELRGI AFDTMLESYI LNSVAGRHDH DSLAERWLKH
451 KTITFEEIAG KGKNQLTFNQ IALEEAGRYA AEDADVTLOL HLKMWPDLOK
501 HKGPLNVFEN IEMPLVPVLS RIERNGVRDL VAYLRALSLE VAEIARLEA
551 EVFRLAGHPF NLNSRDQLER VLFDELGLPA IGKTEKTGKR STSAAVLEAL
601 REAHPIVEKI LQYRELTKLK STYIDPLPDL IHPRTGRLHT RFNQATATATG
651 RLSSSDPNLQ NIPVRTPLGQ RIRRAFIAEE GWLLVALDYS QIELRVLAHL
701 SGDENLIRVF QEGRDIHTET ASWMFGVPRE AVDPLMRRAA KTFNFGVLYG
751 MSAHRLSQEL AIPYEEAQAF IERYFQSFPK VRAWIEKTLE EGRRRGYVET
801 LFGRRRYVPD LEARVKSURE AAERMAFNMP VQGTADLMK LAMVKLFPRL
851 EEMGARMLLQ VHDELVLLEP KERAFAVARL AKEVMEGVYP LAVPLEVEVG
901 IGEDWLSAKE

Figure 3/1
SEQ ID No.: 3

DNA sequence:

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1  ATGAGGGGCT CGCATCACCA TCACCATCAC GCTGCTGACG ATGACGATAA
51  AATGAGGGGC ATGCTACCGC TATTGAGCC CAAGGGCCGG GTCCTCCTGG
101 TCGACGGCCA CCACCTGGCC TACCGCACCT TCCACGCCCT GAAGGGCCTC
151 ACCACCAGCC GGGGGGAGCC GGTGCAGGCG GTCTACGGCT TCGCCAAGAG
201 CCTCCTCAAG GCCCTCAAGG AGGACGGGGA CGCGGTGATC GTGGTCTTTG
251 ACGCCAAGGC CCCCTCCTTC CGCCACGAGG CCTACGGGGG GTACAAGGCG
301 GGCCGGGCCC CCACGCCGGA GGA CTTTCCC CGGCAACTCG CCCTCATCAA
351 GGAGCTGGTG GACCTCCTGG GGCTGGCGCG CCTCGAGGTC CCGGGCTACG
401 AGGCGGACGA CGTCTGGGCC AGCCTGGCCA AGAAGGCGGA AAAGGAGGGC
451 TACGAGGTCC GCATCCTCAC CGCCGACAAA GACCTTTACC AGCTCCTTTC
501 CGACCGCATC CACGTCCTCC ACCCGGAGGG GTACCTCATC ACCCGGCCCT
551 GGCTTTGGGA AAAGTACGGC CTGAGGCCCG ACCAGTGGGC GACTACCGG
601 GCCCTGACCG GGGACGAGTC CGACAACCTT CCCGGGGTCA AGGGCATCGG
651 GGAGAAGACG GCGAGGAAGC TTCTGGAGGA GTGGGGGAGC CTGGAAGCCC
701 TCCTCAAGAA CCTGGACCGG CTGAAGCCCG CCATCCGGGA GAAGATCCTG
751 GCCCACATGG ACGATCTGAA GCTCTCCTGG GACCTGGCCA AGGTGCGCAC
801 CGACCTGCCC CTGGAGGTGG ACTTCGCCAA AAGGCGGGAG CCCGACCGGG
851 AGAGGCTTAG GGCTTTCTG GAGAGGCTTG AGTTTGCGAG CCTCCTCCAC
901 GAGTTCGGCC TTCTGGAAAG CCCCCCGTT GGATACAGAA TAGTGAAAGA
951 CCTGGTGAA TTTGAAAAAC TCATAGAGAA ACTGAGAGAA TCCCTTCGT
1001 TCGCCATAGA TCTTGAGACG TCTTCCCTCG ATCCTTTCGA CTGCGACATT
1051 GTCGGTATCT CTGTGTCTTT CAAACCAAAG GAAGCGTACT ACATACCACT
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1151 TAAAAGAAAT CCTGGAGGAC CCCGGAGCAA AGATCGTTGG TCAGAATTTG
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1251 TCACTTCGAC ACGATGATAG CGGCTTACCT TCTTGAGCCG AACGAAAAGA
1301 AGTTCAATCT GGACGATCTC GCATTGAAAT TTCTTGATA CAAATGACC
1351 TCTTACCAGG AACTCATGTC CTTCTCTTCT CCGCTGTTTG GTTTCAGTTT
1401 TGCCGATGTT CTTGTAGAAA AAGCAGCGAA CTATTCCTGT GAAGATGCCG
1451 ACATCACCTA CAGACTCTAC AAGATCCTGA GCTTAAACT CCACGAGGAG
1501 AGGCTCCTTT GGCTTTACCG GGAGGTGGAG AGGCCCTTT CCGCTGTCCT
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1601 CCTTGTCCTT GGAGGTGGCC GAGGAGATCG CCCGCTCGA GGCAGAGGTC
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1701 AAGGTCCTC TTTGACGAGC TAGGGCTTCC CGCCATCGGC AAGACGGAGA
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1801 GCCCACCCA TCGTGGAGAA GATCCTGCAG TACCGGAGC TCACCAAGCT
1851 GAAGAGACC TACATTGACC CCTTGCCGGA CCTCATCCAC CCCAGGACGG
1901 GCCGCCTCCA CACCCGCTTC AACCAGACGG CCACGGCCAC GGGCAGGCTA
1951 AGTAGCTCCG ATCCCAACCT CCAGAACATC CCCGTCCGCA CCCCCTTGG
2001 GCAGAGGATC CGCCGGGCCT TCATCGCCGA GGAGGGGTGG CTATTGGTGG
2051 CCCTGGACTA TAGCCAGATA GAGCTCAGGG TGCTGGCCCA CCTCTCCGGC
2101 GACGAGAACC TGATCCGGGT CTTCCAGGAG GGGCGGGACA TCCACACGGA
2151 GACCGCCAGC TGGATGTTG GCGTCCCCG GGAGGCCGTG GACCCCTGA
2201 TGCGCCGGGC GGCCAAGACC ATCAACTTCG GGGTCCTCTA CGGCATGTCG
2251 GCCACCGCC TCTCCAGGA GCTAGCCATC CTTACGAGG AGGCCAGGC
2301 CTTCAATTGAG CGCTACTTTC AGAGCTTCCC CAAGGTGCGG GCCTGGATTG
2351 AGAAGACCTT GGAGGAGGGC AGGAGGCGGG GGTACGTGGA GACCTCTTC
2401 GGCCGCCGCC GCTACGTGCC AGACCTAGAG GCGCGGTGA AGAGCGTGG
2451 GGAGGCGGCC GAGCGCATGG CCTTCAACAT GCGCGTCCAG GGCACCGCCG
2501 CCGACCTCAT GAAGCTGGCT ATGGTGAAGC TCTTCCCCAG GCTGGAGGAA

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Figure 3/2
SEQ ID No.: 3

2551 ATGGGGGCCA GGATGCTCCT TCAGGTCCAC GACGAGCTGG TCCTCGAGGC
2601 CCCAAAAGAG AGGGCGGAGG CCGTGGCCCG GCTGGCCAAG GAGGTCATGG
2651 AGGGGGTGTA TCCCCTGGCC GTGCCCCTGG AGGTGGAGGT GGGGATAGGG
2701 GAGGACTGGC TCTCCGCCAA GGAGTGA

SEQ ID No.: 9

amino acid sequence:

1 MRGSHHHHHH AADDDDKMRG MLPLFEPKGR VLLVDGHHLA YRTFHALKGL
51 TTSRGEVPQA VYGFAKSLLK ALKEDGDAVI VVFDKAPSF RHEAYGGYKA
101 GRAPTPEDFP RQLALIKELV DLLGLARLEV PGYEADDVLA SLAKKAEKEG
151 YEVRILTADK DLYQLLSDRI HVLHPEGYLI TPWLWEKYG LRPDQWADYR
201 ALTGDESDNL PGVKGIGECT ARKLEEWGS LEALLKNLDR LKPAIREKIL
251 AHMDDLKLSW DLAKVRTDLP LEVDFAKRRE PDRERLRAFL ERLEFGSLLH
301 EFGLLESPPV GYRIVKDLVE FEKLIEKLRE SPSFAIDLET SSLDPFDCCI
351 VGISVSFKPK EAYYIPLHHR NAQNLDEKEV LKKLKEILED PGAKIVGQNL
401 KFDYKVLNVK GVEPVPPHFD TMIAAYLLEP NEKKFNLDL ALKFLGYKMT
451 SYQELMSFSS PLFGFSFADV PVEKAANYSC EDADITYRLY KILSLKLHEE
501 RLLWLYREVE RPLSAVLAHM EATGVRLDVA YLRALSLEVA EEIARLEAEV
551 FRLAGHPFNL NSRDQLERVL FDELGLPAIG KTEKTGKRST SAAVLEALRE
601 AHPIVEKILQ YRELTKLKST YIDPLPLIH PRTGRLHTRF NQTATATGRL
651 SSSDPNLQNI PVRTPLGQRI RRAFIAEEGW LLVALDYSQI ELRVLAHLG
701 DENLIRVFQE GRDIHTETAS WMFGVPREAV DPLMRRAAKT INFGVLYGMS
751 AHRLSQELAI PYEEAQAFIE RYFQSFPKVR AWIEKTLEEG RRRGYVETLF
801 GRRRYVPDLE ARVKSUREAA ERMAFNMPVQ GTAADLMKLA MVKLFPRLEE
851 MGARMLLQVH DELVLEAPKE RAEAVARLAK EVMEGVYPLA VPLEVEVGIG
901 EDWLSAKE

Figure 4/1
SEQ ID No.: 4

DNA sequence:

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1  ATGAGGGGCT CGCATCACCA TCACCATCAC GCTGCTGACG ATGACGATAA
51 AATGAGGGGC ATGCTACCGC TATTTGAGCC CAAGGGCCGG GTCCTCCTGG
101 TCGACGGCCA CCACCTGGCC TACCGCACCT TCCACGCCCT GAAGGGCCTC
151 ACCACCAGCC GGGGGGAGCC GGTGCAGGCG GTCTACGGCT TCGCCAAGAG
201 CCTCCTCAAG GCCCTCAAGG AGGACGGGGA CGCGGTGATC GTGGTCTTTG
251 ACGCCAAGGC CCCCTCCTTC CGCCACGAGG CCTACGGGGG GTACAAGGCG
301 GGCCGGGCCC CCACGCCGGA GGACTTTCCC CGGCAACTCG CCCTCATCAA
351 GGAGCTGGTG GACCTCCTGG GGCTGGCGCG CCTCGAGGTC CCGGGCTACG
401 AGGCGGACGA CGTCCTGGCC AGCCTGGCCA AGAAGGCGGA AAAGGAGGGC
451 TACGAGGTCC GCATCCTCAC CGCCGACAAA GACCTTTACC AGCTCCTTTC
501 CGACCGCATC CACGTCTCTC ACCCCGAGGG GTACCTCATC ACCCCGGCCT
551 GGCTTTGGGA AAAGTACGGC CTGAGGCCCC ACCAGTGGGC CGACTACCGG
601 GCCCTGACCG GGGACGAGTC CGACAACCTT CCCGGGGTCA AGGGCATCGG
651 GGAGAAGACG GCGAGGAAGC TTCTGGAGGA GTGGGGGAGC CTGGAAGCCC
701 TCCTCAAGAA CCTGGACCGG CTGAAGCCCG CCATCCGGGA GAAGATCCTG
751 GCCACATGG ACGATCTGAA GCTCTCCTGG GACCTGGCCA AGGTGCGCAC
801 CGACCTGCCC CTGGAGGTGG ACTTCGCCAA AAGGCGGGAG CCCGACCGGG
851 AGAGGCTTAG GGCCTTTCTG GAGAGGCTTG AGTTTGGCAG CCTCCTCCAC
901 GAGTTCGGCC TTCTGGAAAG CCCCCCGTT GGATACAGAA TAGTGAAAGA
951 CCTGGTGGAA TTTGAAAAAC TCATAGAGAA ACTGAGAGAA TCCCCTTCGT
1001 TCGCCATAGA TCTTGAGACG TCTTCCCTCG ATCCTTTCGA CTGCGACATT
1051 GTCGGTATCT CTGTGTCTTT CAAACCAAAG GAAGCGTACT ACATACCACT
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1151 TAAAAGAAAT CCTGGAGGAC CCCGGAGCAA AGATCGTTGG TCAGAATTG
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1601 CCTTGTCCTT GGAGGTGGCC GAGGAGATCG CCCGCCTCGA GGCCGAGGTC
1651 TTCCGCCTGG CCGGCCACCC CTTCAACCTC AACTCCCGGG ACCAGCTGGA
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1801 GCCACCCCA TCGTGGAGAA GATCCTGCAG TACCGGGAGC TCACCAAGCT
1851 GAAGAGCACC TACATTGACC CTTGCCGGA CCTCATCCAC CCCAGGACGG
1901 GCCGCCTCCA CACCCGCTTC AACCAGACGG CCACGGCCAC GGGCAGGCTA
1951 AGTAGCTCCG ATCCCAACCT CCAGAACATC CCCGTCCGCA CCCCGCTTGG
2001 GCAGAGGATC CGCCGGGCTT TCATCGCCGA GGAGGGGTGG CTATTGGTGG
2051 CCCTGGACTA TAGCCAGATA GAGCTCAGGG TGCTGGCCCA CCTCTCCGGC
2101 GACGAGAACC TGATCCGGGT CTTCCAGGAG GGGCGGGACA TCCACACGGA
2151 GACCGCCAGC TGGATGTTCT GCGTCCCCCG GGAGGCCGTG GACCCCTGA
2201 TGCGCCGGGC GGCCAAGACC ATCAACTTCG GGGTCCTCTA CGGCATGTCTG
2251 GCCACCGCC TCTCCAGGA GCTAGCCATC CCTTACGAGG AGGCCAGGC
2301 CTTCATTGAG CGTACTTTC AGAGCTTCCC CAAGGTGCGG GCCTGGATTG
2351 AGAAGACCTT GGAGGAGGGC AGGAGGCGGG GGTACGTGGA GACCCTCTTC
2401 GGCCGCCGCC GCTACGTGCC AGACCTAGAG GCCCGGGTGA AGAGCGTGCG
2451 GGAGGCGGCC GAGCGCATGG CTTCAACAT GCCCGTCCAG GGCACCGCCG
2501 CCGACCTCAT GAAGCTGGCT ATGGTGAAGC TCTTCCCAG GCTGGAGGAA

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Figure 4/2
SEQ ID No.: 4

2551 ATGGGGGCCA GGATGCTCCT TCAGGTCCAC GACGAGCTGG TCCTCGAGGC
2601 CCCAAAAGAG AGGGCGGAGG CCGTGGCCCCG GCTGGCCAAG GAGGTCATGG
2651 AGGGGGTGTA TCCCCTGGCC GTGCCCTGG AGGTGGAGGT GGGGATAGGG
2701 GAGGACTGGC TCTCCGCCAA GGAGTGA

SEQ ID NO.: 10

amino acid sequence:

1 MRGSHHHHHH AADDDDKMRG MLPLFEPKGR VLLVDGHHLA YRTFHALKGL
51 TTSRGEVPQA VYGFAKSLLK ALKEDGDAVI VVFDKAPSF RHEAYGGYKA
101 GRAPTPEDFP RQLALIKELV DLLGLARLEV PGYEADDVLA SLAKKAEKEG
151 YEVRILTADK DLYQLLSDRI HVLHPEGYLI TPAWLWEKYG LRPDQWADYR
201 ALTGDESDNL PGVKGIGECT ARKLLEEWGS LEALLKNLDR LKPAIREKIL
251 AHMDDLKLSW DLAKVRTDLP LEVDFAKRRE PDRERLRAFL ERLEFGSLLH
301 EFGLLESPPV **GYRIVKDLVE FEKLEKLE SPSFAIDLET SSLDPFDCHI**
351 VGISVSFKPK EAYYIPLHHR NAQNLDEKEV LKKLKEILED PGAKIVGQNL
401 KFDYKVLNVK GVEPVPPHFD TMIAAYLLEP NEKKFNLDDL ALKFLGYKMT
451 SYQELMSFSS PLFGFSFADV PVEKAANYSC EDADITYRLY KILSLKLHEA
501 **DLENVFKIE MPLVSVLARM ELNGVRLDVA YLRALSLEVA EEIARLEAEV**
551 FRLAGHPFNL NSRDQLERVL FDELGLPAIG KTEKTGKRST SAAVLEALRE
601 AHPIVEKILQ YRELTCLKST YIDPLPLIH PRTGRLHTRF NQTATATGRL
651 SSSDPNLQNI PVRTPLGQRI RRAFIAEEGW LLVALDYSQI ELRVLAHLGS
701 DENLIRVFQE GRDIHTETAS WMFGVPREAV DPLMRRAAKT INFGVLYGMS
751 AHRLSQELAI PYEEAQAFIE RYFQSFPKVR AWIEKTLEEG RRRGYVETLF
801 GRRRYVPDLE ARVKSUREAA ERMAFNMPVQ GTAADLMKLA MVKLFPRLEE
851 MGARMLLQVH DELVLEAPKE RAEAVARLAK EVMEGVYPLA VPLEVEVGIG
901 EDWLSAKE

Figure 5/1
SEQ ID No.: 5

DNA sequence:

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1  ATGAGGGGCT CGCATCACCA TCACCATCAC GCTGCTGACG ATGACGATAA
51 AATGAGGGGC ATGCTACCGC TATTTGAGCC CAAGGGCCGG GTCCTCCTGG
101 TCGACGGCCA CCACCTGGCC TACCGCACCT TCCACGCCCT GAAGGGCCCTC
151 ACCACCAGCC GGGGGGAGCC GGTGCAGGCG GTCTACGGCT TCGCCAAGAG
201 CCTCCTCAAG GCCCTCAAGG AGGACGGGGA CGCGGTGATC GTGGTCTTTG
251 ACGCCAAGGC CCCCTCCTTC CGCCACGAGG CCTACGGGGG GTACAAGGCG
301 GGCCGGGCCC CCACGCCGGA GGACTTTCCC CGGCAACTCG CCCTCATCAA
351 GGAGCTGGTG GACCTCCTGG GGCTGGCGCG CCTCGAGGTC CCGGGCTACG
401 AGGCGGACGA CGTCTGGGCC AGCCTGGCCA AGAAGGCGGA AAAGGAGGGC
451 TACGAGGTCC GCATCCTCAC CGCCGACAAA GACCTTTACC AGCTCCTTTC
501 CGACCGCATC CACGTCTCTC ACCCCGAGGG GTACCTCATC ACCCCGGCCT
551 GGCTTTGGGA AAAGTACGGC CTGAGGCCCC ACCAGTGGGC CGACTACCGG
601 GCCCTGACCG GGGACGAGTC CGACAACCTT CCCGGGGTCA AGGGCATCGG
651 GGAGAAGACG GCGAGGAAGC TTCTGGAGGA GTGGGGGAGC CTGGAAGCCC
701 TCCTCAAGAA CCTGGACCGG CTGAAGCCCG CCATCCGGGA GAAGATCCTG
751 GCCCACATGG ACGATCTGAA GCTCTCCTGG GACCTGGCCA AGGTGCGCAC
801 CGACCTGCCC CTGGAGGTGG ACTTCGCCAA AAGGCGGGAG CCCGACCGGG
851 AGAGGCTTAG GGCTTTCTG GAGAGGCTTG AGTTTGGCAG CCTCCTCCAC
901 GAGTTCGGCC TTCTGGAAAG CCCCCATCCA GCAGTTGTGG ACATCTTCGA
951 ATACGATATT CCATTTGCAA AGAGATACCT CATCGACAAA GGCCTAATAC
1001 CAATGGAGGG GGAAGAAGAG CTAAGATTTC TTGCCTTCGA TATAGAAACC
1051 CTCTATCACG AAGGAGAAGA GTTTGGAAAA GGCCCAATTA TAATGATTAG
1101 TTATGCAGAT GAAAATGAAG CAAAGGTGAT TACTTGAAA AACATAGATC
1151 TTCCATACGT TGAGGTTGTA TCAAGCGAGA GAGAGATGAT AAAGAGATTT
1201 CTCAGGATTA TCAGGGAGAA GGATCCTGAC ATTATAGTTA CTTATAATGG
1251 AGACTCATTC GACTTCCCAT ATTTAGCGAA AAGGGCAGAA AAACCTGGGA
1301 TTAAATTAAC CATTGGAAGA GATGGAAGCG AGCCCAAGAT GCAGAGAATA
1351 GGCGATATGA CGGCTGTAGA AGTCAAGGGA AGAATACATT TCGACTTGTA
1401 TCATGTAATA ACAAGGACAA TAAATCTCCC AACATACACA CTAGAGGCTG
1451 TATATGAAGC AATTTTTTGA AAGCCAAAGG AGAAGGTATA CGCCGACGAG
1501 ATAGCAAAAG CCTGGGAAAG TGGAGAGAAC CTTGAGAGAG TTGCCAAATA
1551 CTCGATGGAA GATGCAAAGG CAACTTATGA ACTCGGGAAA GAATTCCTTC
1601 CAATGGAAAT TCAGCTTTCA GAGAGGCTCC TTTGGCTTTA CCGGGAGGTG
1651 GAGAGGCCCC TTTCCGCTGT CCTGGCCCAC ATGGAGGCCA CGGGGGTGCG
1701 CCTGGACGTG GCCTATCTCA GGGCCTTGTC CCTGGAGGTG GCCGAGGAGA
1751 TCGCCCGCCT CGAGGCCGAG GTCTTCCGCC TGGCCGGCCA CCCCTTCAAC
1801 CTCAACTCCC GGGACCAGCT GGAAAGGGTC CTCTTTGACG AGCTAGGGCT
1851 TCCCGCCATC GGCAAGACGG AGAAGACCGG CAAGCGCTCC ACCAGCGCCG
1901 CCGTCCTGGA GGCCCTCCGC GAGGCCACCC CCATCGTGGA GAAGATCCTG
1951 CAGTACCGGG AGCTACACAA GCTGAAGAGC ACCTACATTG ACCCCTTGCC
2001 GGACCTCATC CACCCCAGGA CGGGCCGCCT CCACACCCGC TTCAACCAGA
2051 CGGCCACGGC CACGGGCAGG CTAAGTAGCT CCGATCCCAA CCTCCAGAAC
2101 ATCCCCGTCC GCACCCCGCT TGGGCAGAGG ATCCGCCGGG CCTTCATCGC
2151 CGAGGAGGGG TGCTATTGG TGGCCCTGGA CTATAGCCAG ATAGAGCTCA
2201 GGGTGCTGGC CCACCTCTCC GGCGACGAGA ACCTGATCCG GGTCTTCCAG
2251 GAGGGGCGGG ACATCCACAC GGAGACCGCC AGCTGGATGT TCGGCGTCCC
2301 CCGGGAGGCC GTGGACCCCC TGATGCGCCG GGCGGCCAAG ACCATCAACT
2351 TCGGGGTCCT CTACGGCATG TCGGCCACC GCCTCTCCA GGAGCTAGCC
2401 ATCCCTTACG AGGAGGCCCA GGCTTCATT GAGCGCTACT TTCAGAGCTT
2451 CCCCAGGTG CGGGCCTGGA TTGAGAAGAC CCTGGAGGAG GGCAGGAGGC
2501 GGGGGTACGT GGAGACCCTC TTCGGCCGCC GCCGCTACGT GCCAGACCTA

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Figure 5/2
SEQ ID No.: 5

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2551 GAGGCCCGGG TGAAGAGCGT GCGGGAGGCG GCCGAGCGCA TGGCCTTCAA
2601 CATGCCCGTC CAGGGCACCG CCGCCGACCT CATGAAGCTG GCTATGGTGA
2651 AGCTCTTCCC CAGGCTGGAG GAAATGGGGG CCAGGATGCT CCTTCAGGTC
2701 CACGACGAGC TGGTCCTCGA GGCCCCAAAA GAGAGGGCGG AGGCCGTGGC
2751 CCGGCTGGCC AAGGAGGTCA TGGAGGGGGT GTATCCCCTG GCCGTGCCCC
2801 TGGAGGTGGA GGTGGGGATA GGGGAGGACT GGCTCTCCGC CAAGGAGTGA

```

SEQ ID No.: 11

amino acid sequence:

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1  MRGSHHHHHH AADDDDKMRG MLPLFEPKGR VLLVDGHHLA YRTFHALKGL
51  TTSRGEVPQA VYGFAKSLK ALKEDGDAVI VVFDKAPSF RHEAYGGYKA
101 GRAPTPEDFP RQLALIKELV DLLGLARLEV PGYEADDVLA SLAKKAEKEG
151 YEVRILTADK DLYQLLSMRI HVLHPEGYLI TPAWLWEKYG LRPDQWADYR
201 ALTGDESDNL PGVKGIGKEK ARKLLEEWGS LEALLKNLDR LKPAIREKIL
251 AHMDDLKLSW DLAKVRTDLP LEVDFAKRRE PDRERLRAFL ERLEFGSLLH
301 EFGLESPPH AVVDIFEYDI PFAKRYLIDK GLIPMEGEEE LKILAFDIET
351 LYHEGEEFGK GPIIMISYAD ENEAKVITWK NIDLPYVEVV SSEREMIKRF
401 LRIIREKDPD IIVTYNGDSF DFPYLAKRAE KLGIKLTIGR DGSEPKMQRI
451 GDMTAVEVKG RIHFDLYHVI TRTINLPTYT LEAVYEAIFG KPKEKVYADE
501 IAKAWESGEN LERVAKYSME DAKATYELGK EFLPMEIQLS ERLLWLYREV
551 ERPLSAVLAH MEATGVRLDV AYLRLSLEV AEEIARLEAE VFRLAGHPFN
601 LNSRDQLERV LFDELGLPAI GKTEKTGKRS TSAAVLEALR EAHPIVEKIL
651 QYRELTKLKS TYIDPLPDLI HPRTGRLHTR FNQTATATGR LSSSDPNLQN
701 IPVRTPLGQR IRRAFIAEEG WLLVALDYSQ IELRVLAHLS GDENLIRVFQ
751 EGRDIHTETA SWMFGVPREA VDPLMRRAAK TINFGVLYGM SAHRLSQELA
801 IPYEEAQAFI ERYFQSFPKV RAWIEKTEE GRRRGYVETL FGRRRYVPDL
851 EARVKSUREA AERMAFNMPV QGTAADLMKL AMVKLFPRLE EMGARMMLQV
901 HDELVLAPK ERAEAVARLA KEVMEGVYPL AVPLEVEVGI GEDWLSAKE*

```

Figure 6/1
SEQ ID No.: 6

DNA sequence:

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1   ATGAGGGGCT CGCATCACCA TCACCATCAC GCTGCTGACG ATGACGATAA
51  AATGAGGGGC ATGCTACCGC TATTTGAGCC CAAGGGCCCGG GTCCTCCTGG
101 TCGACGGCCA CCACCTGGCC TACCGCACCT TCCACGCCCT GAAGGGCCTC
151 ACCACCAGCC GGGGGGAGCC GGTGCAGGCG GTCTACGGCT TCGCCAAGAG
201 CCTCCTCAAG GCCCTCAAGG AGGACGGGGA CGCGGTGATC GTGGTCTTTG
251 ACGCCAAGGC CCCCTCCTTC CGCCACGAGG CCTACGGGGG GTACAAGGCG
301 GGCCGGGCCC CCACGCCGGA GGACTTTCCC CGGCAACTCG CCCTCATCAA
351 GGAGCTGGTG GACCTCCTGG GGCTGGCGCG CCTCGAGGTC CCGGGCTACG
401 AGGCGGACGA CGTCTGGGCC AGCCTGGCCA AGAAGGCGGA AAAGGAGGGC
451 TACGAGGTCC GCATCCTCAC CGCCGACAAA GACCTTTACC AGCTCCTTTC
501 CGACCGCATC CACGTCTCTC ACCCCGAGGG GTACCTCATC ACCCCGGCCT
551 GGCTTTGGGA AAAGTACGGC CTGAGGCCCG ACCAGTGGGC CGACTACCGG
601 GCCCTGACCG GGGACGAGTC CGACAACCTT CCCGGGGTCA AGGGCATCGG
651 GGAGAAGACG GCGAGGAAGC TTCTGGAGGA GTGGGGGAGC CTGGAAGCCC
701 TCCTCAAGAA CCTGGACCGG CTGAAGCCCG CCATCCGGGA GAAGATCCTG
751 GCCCACATGG ACGATCTGAA GCTCTCCTGG GACCTGGCCA AGGTGCGCAC
801 CGACCTGCCC CTGGAGGTGG ACTTCGCCAA AAGGCGGGAG CCCGACCGGG
851 AGAGGCTTAG GGCCTTTCTG GAGAGGCTTG AGTTTGGCAG CCTCCTCCAC
901 GAGTTCGGCC TTCTGGAAAG CCCC GTTAGA GAACATCCAG CAGTTGTGGA
951 CATCTTCGAA TACGATATTC CATTGTGCAA GAGATACCTC ATCGACAAAG
1001 GCCTAATACC AATGGAGGGG GAAGAAGAGC TAAAGATTCT TGCCTTCGAT
1051 ATAGAAACCC TCTATCACGA AGGAGAAGAG TTTGGAAAAG GCCCAATTAT
1101 AATGATTAGT TATGCAGATG AAAATGAAGC AAAGGTGATT ACTTGGAAAA
1151 ACATAGATCT TCCATACGTT GAGGTGTAT CAAGCGAGAG AGAGATGATA
1201 AAGAGATTTT TCAGGATTAT CAGGGAGAAG GATCCTGACA TTATAGTTAC
1251 TTATAATGGA GACTCATTCG ACTTCCCATA TTAGCGAAA AGGGCAGAAA
1301 AACTTGGGAT TAAATTAACC ATTGGAAGAG ATGGAAGCGA GCCCAAGATG
1351 CAGAGAATAG GCGATATGAC GGCTGTAGAA GTCAAGGGAA GAATACATTT
1401 CGACTTGTAT CATGTAATAA CAAGGACAAT AAATCTCCCA ACATACACAC
1451 TAGAGGCTGT ATATGAAGCA ATTTTGGAA AGCCAAAGGA GAAGGTATAC
1501 GCCGACGAGA TAGCAAAAGC CTGGGAAAGT GGAGAGAACC TTGAGAGAGT
1551 TGCCAAATAC TCGATGGAAG ATGCAAAGGC AACTTATGAA CTCGGGAAAG
1601 AATTCCTTCC AATGGAAATT CAGCTTTCAA GATTAGTTGG ACAACCTTTA
1651 TGGGATGTTT CAAGGTCAAG CACAGGGAAC CTTGTAGAGT GGTTCTTACT
1701 TAGGAAAGCC TACGAAAGAA ACGAAGTAGC TCCAAACAAG CCAAGTGAAG
1751 AGGAGTATCA AAGAAGGCTC AGGGAGAGCT ACACAGGTGG ATTCGTGCGC
1801 CTGGACGTGG CCTATCTCAG GGCCTTGTC CTGGAGGTGG CCGAGGAGAT
1851 CGCCCGCCTC GAGGCCGAGG TCTTCCGCTT GGCCGGCCAC CCCTTCAACC
1901 TCAACTCCCG GGACCAGCTG GAAAGGGTCC TCTTTGACGA GCTAGGGCTT
1951 CCCGCCATCG GCAAGACGGA GAAGACCGGC AAGCGCTCCA CCAGCGCCGC
2001 CGTCCTGGAG GCCCTCCGCG AGGCCCACCC CATCGTGGAG AAGATCCTGC
2051 AGTACCGGGA GCTCACCAAG CTGAAGAGCA CCTACATTGA CCCCTTGCCG
2101 GACCTCATCC ACCCCAGGAC GGGCCGCCTC CACACCCGCT TCAACCAGAC
2151 GGCCACGGCC ACGGGCAGGC TAAGTAGCTC CGATCCCAAC CTCCAGAACA
2201 TCCCCGTCCG CACCCCGCTT GGGCAGAGGA TCCGCCGGGC CTTTCATCGCC
2251 GAGGAGGGGT GGCTATTGGT GGCCCTGGAC TATAGCCAGA TAGAGCTCAG
2301 GGTGCTGGCC CACCTCTCCG GCGACGAGAA CCTGATCCGG GTCTTCCAGG
2351 AGGGGCGGGA CATCCACACG GAGACCGCCA GCTGGATGTT CGGCGTCCCC
2401 CGGGAGGCCG TGGACCCCTT GATGCGCCGG GCGGCAAGA CCATCAACTT
2451 CGGGGTCTCT TACGGCATGT CGGCCACCG CCTCTCCAG GAGCTAGCCA
2501 TCCCTTACGA GGAGGCCAG GCCTTCATTG AGCGCTACTT TCAGAGCTTC

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Figure 6/2
SEQ ID No.: 6

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2551 CCCAAGGTGC GGGCCTGGAT TGAGAAGACC CTGGAGGAGG GCAGGAGGCG
2601 GGGGTACGTG GAGACCCTCT TCGGCCGCCG CCGCTACGTG CCAGACCTAG
2651 AGGCCCGGGT GAAGAGCGTG CGGGAGGCGG CCGAGCGCAT GGCCTTCAAC
2701 ATGCCCGTCC AGGGCACCGC CGCCGACCTC ATGAAGCTGG CTATGGTGAA
2751 GCTCTTCCCC AGGCTGGAGG AAATGGGGGC CAGGATGCTC CTTCAGGTCC
2801 ACGACGAGCT GGTCTTCGAG GCCCAAAG AGAGGGCGGA GGCCGTGGCC
2851 CGGCTGGCCA AGGAGGTCAT GGAGGGGGTG TATCCCCTGG CCGTGCCCCCT
2901 GGAGGTGGAG GTGGGGATAG GGGAGGACTG GCTCTCCGCC AAGGAGTGA

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SEQ ID No.: 12

amino acid sequence:

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1 MRGSHHHHHH AADDDDKMRG MLPLFEPKGR VLLVDGHHLA YRTFHALKGL
51 TTSRGEVQQA VYGFAKSLK ALKEDGDAVI VVFDKAPSF RHEAYGGYKA
101 GRAPTPEDFP RQLALIKELV DLLGLARLEV PGYEADDVLA SLAKKAEKEG
151 YEVRILTADK DLYQLSDRI HVLHPEGYLI TPAWLWEKYG LRPDQWADYR
201 ALTGDESDNL PGVKGIGECT ARKLEEWGS LEALLKNLDR LKPAIREKIL
251 AHMDDLKLSW DLAKVRTDLP LEVDFAKRRE PDRERLRAFL ERLEFGSLH
301 EFGLLESPVR EHPAVVDIFE YDIPFAKRYL IDKGLIPMEG EEELKILAFD
351 IETLYHEGEE FGKGPIIMIS YADENEAKVI TWKNIDLPIV EVVSSEREMI
401 KRFLRIIREK DPDIIVTYNG DSFDFFPYLAK RAEKLGIKLT IGRDGSEPKM
451 QRIGDMTAVE VKGRIHFDLY HVITRTINLP TYTLEAVYEA IFGKPKEKVY
501 ADEIAKAWES GENLERVAKY SMEDAKATYE LGKEFLPMEI QLSRLVGQPL
551 WDVSRSSSTGN LVEWFLLRKA YERNEVAPNK PSEEEYQRRL RESYTGGFVR
601 LDVAYLRALS LEVAEEIARL EAEVFRLAGH PFNLNSRDQL ERVLFDELGL
651 PAIGKTEKTG KRSTSAAVLE ALREAHPIVE KILQYRELTK LKSTYIDPLP
701 DLIHPRTGRL HTRFNQTATA TGRLLSSSDPN LQNIPTVRTPL GQIRIRAFIA
751 EEGWLLVALD YSQIELRVLA HLSGDNELIR VFQEGRDIHT ETASWMFGVP
801 REAVDPLMRR AAKTINFGVL YGMSAHRSLQ ELAIPYEEAQ AFIERYFQSF
851 PKVRAWIEKT LEEGRRRGYV ETLFGRRRYV PDLEARVKS SV REAAERMAFN
901 MPVQGTAADL MKLAMVKLFP RLEEMGARM LQVHDELVL E APKERAEAVA
951 RLAKEVMEGV YPLAVPLEVE VGIGEDWLSA KE*

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Figure 7

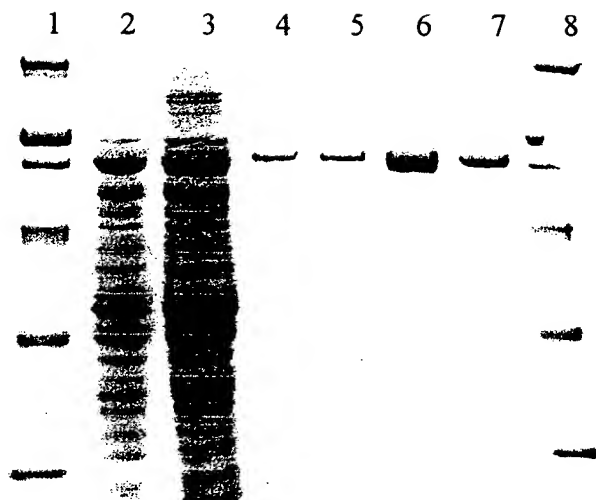


Figure 8

09/623326

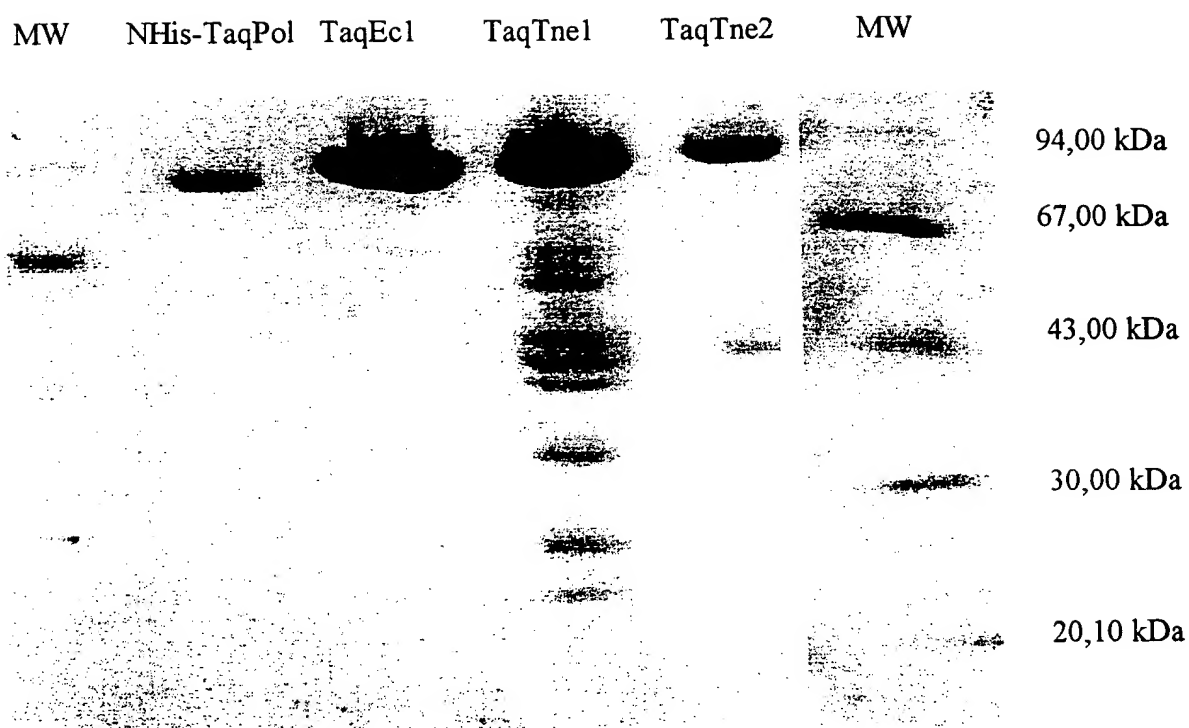


Figure 9

09/623326

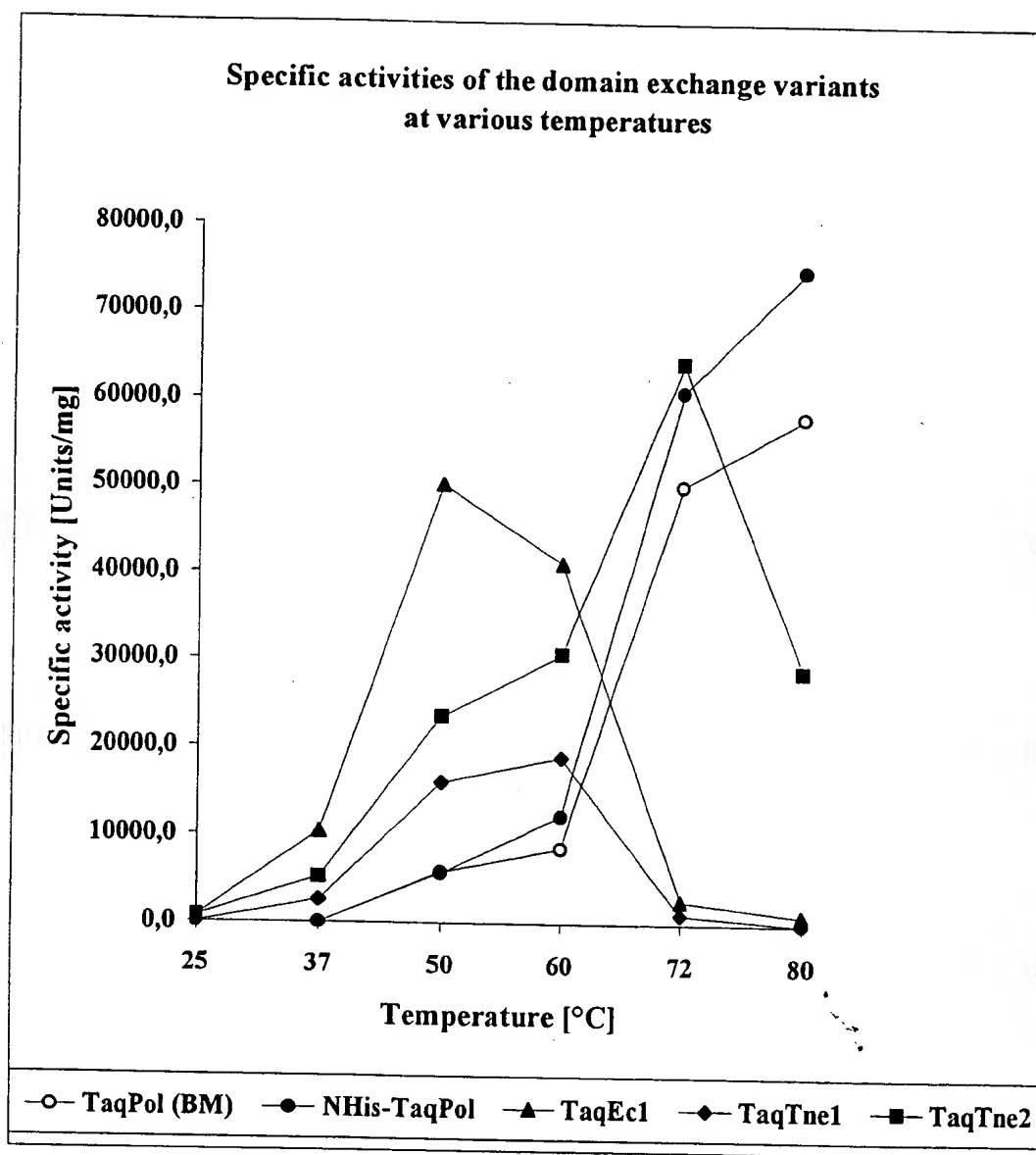


Figure 10

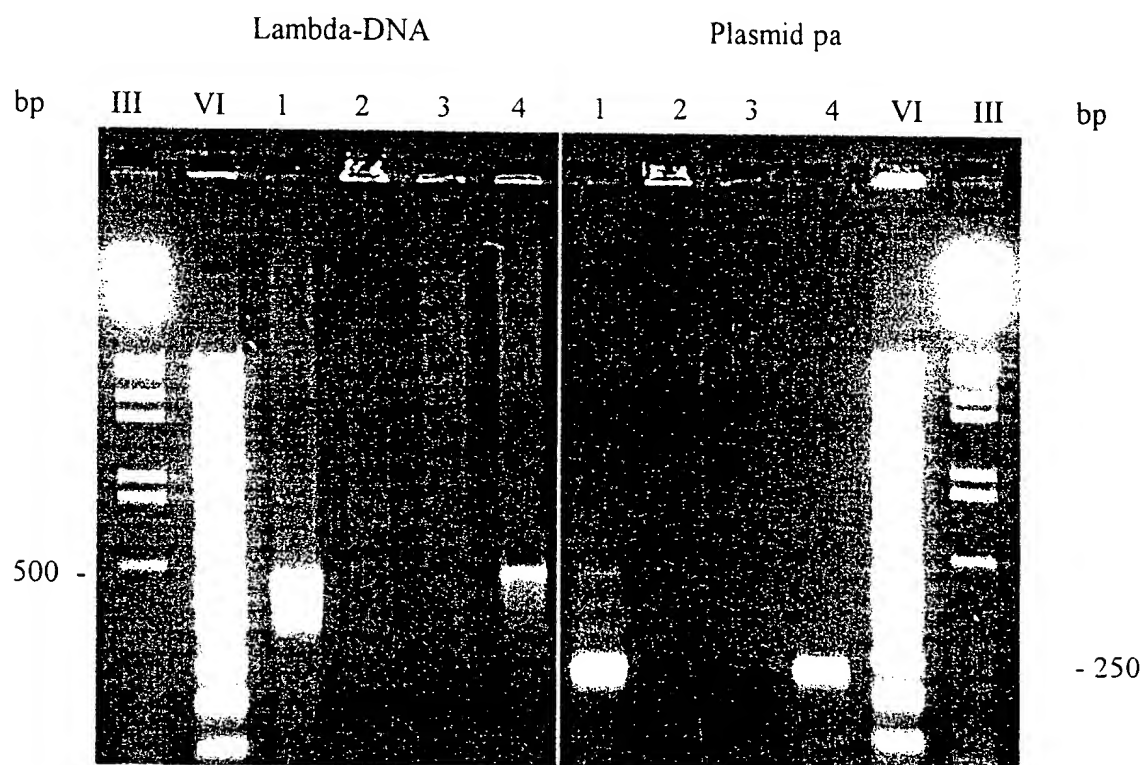


Figure 11

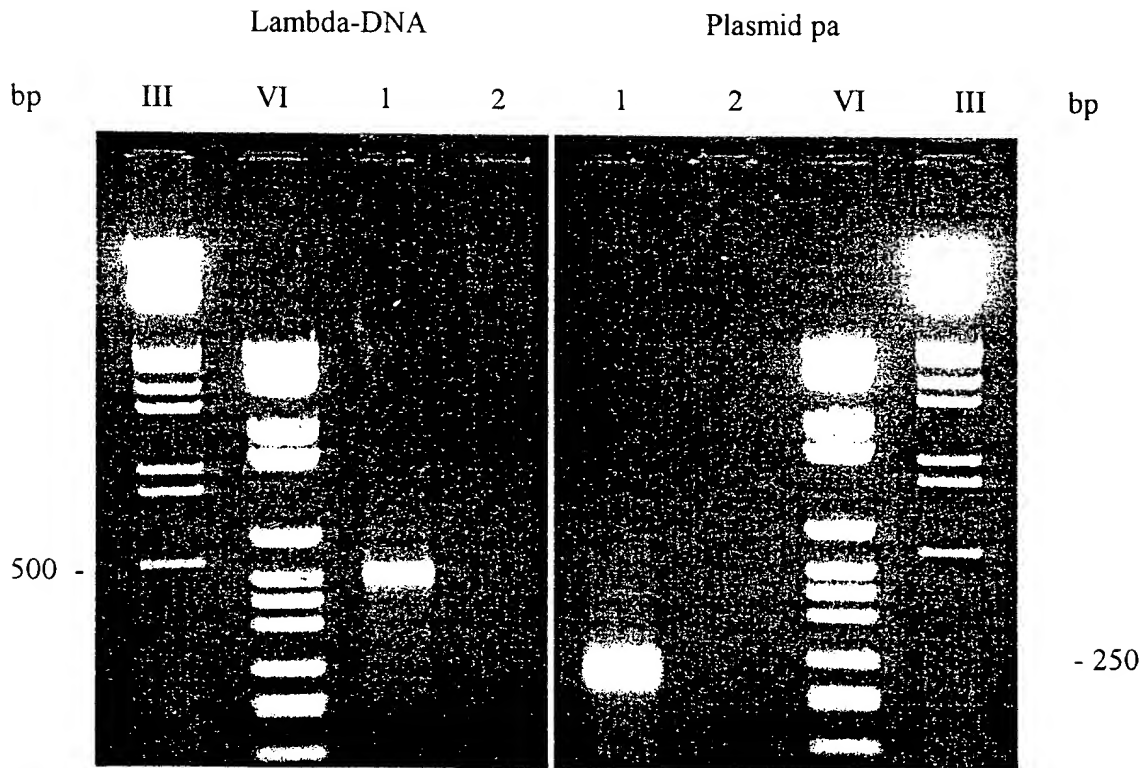
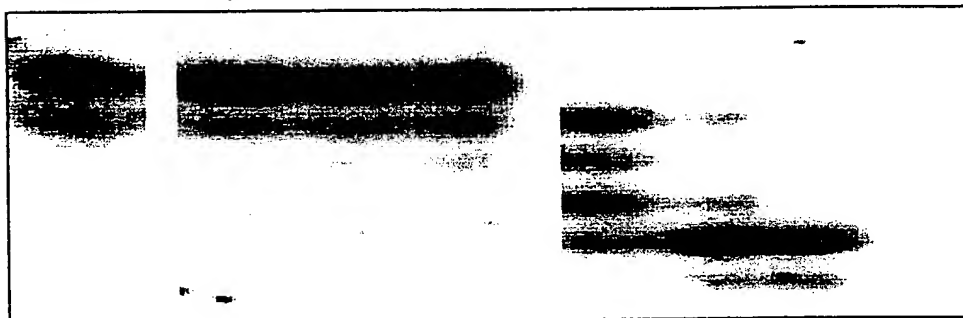


Figure 12

09/623326

without pol. NHisTaqPol (500 U/ μ l) UITma DNA Polymerase (5U/ μ l)

20 h 0,5 h 3 h 20 h 1 min 5 min 10 min 20 h



- 23 mer

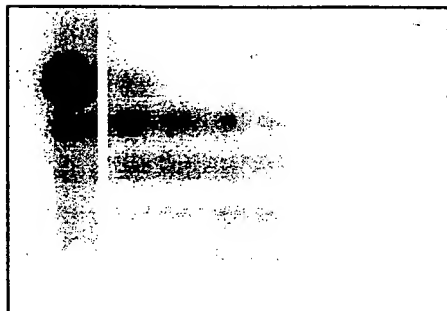
- 20 mer

Figure 13

09/623326

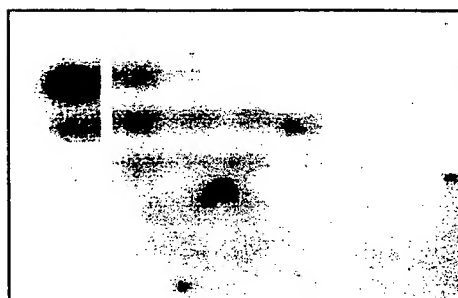
without pol. TaqEc1 (500 U/ μ l)

600 15 30 45 60 90 180 600 min



ohne Pol TaqEc1 (500 U/ μ l)

600 15 30 45 60 90 180 600 min



- 23 mer

- 20 mer

Figure 14

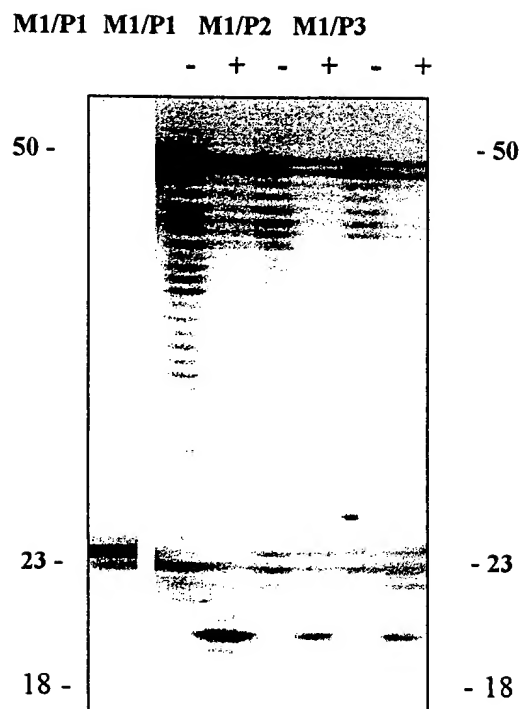


Figure 15

Degradation of primers at the 3'-end (3'-5' exonuclease assay)
and
Correction of 3'-mismatched Primers and their extension (3'-mismatch primer correction assay)

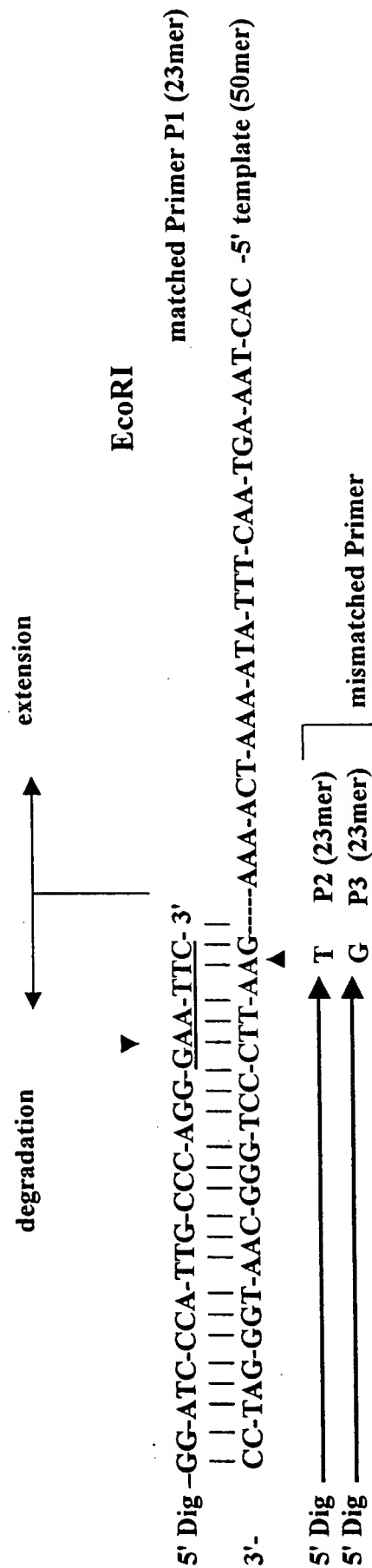


Figure 16

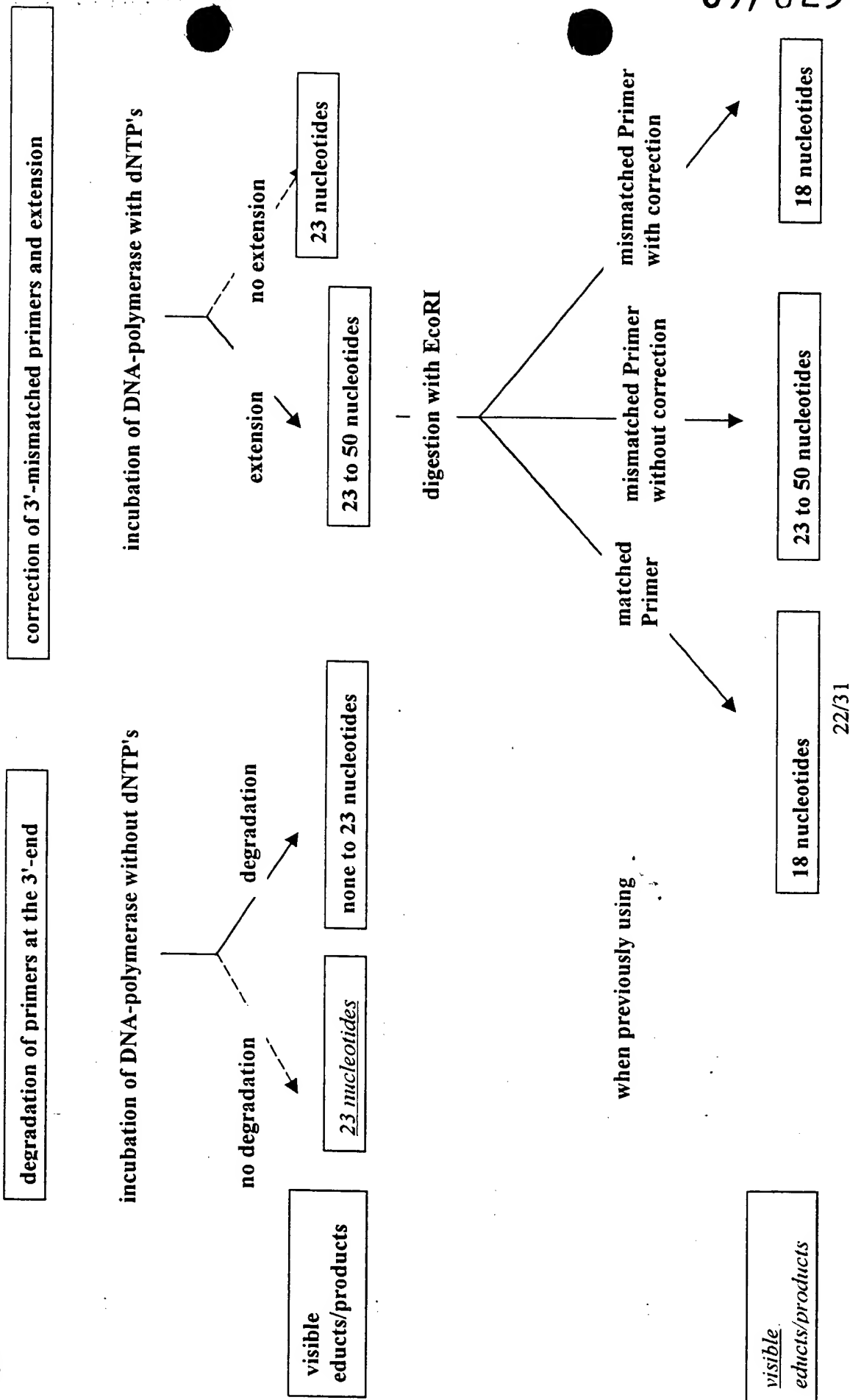


Fig. 17/1

SEQ ID No. 43
 SEQ ID No. 44
 SEQ ID No. 45
 SEQ ID No. 46

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chimera_____ ----MARLFLFDGTALAYRAYYALDRSLSTSTGIPTNATYGVARMLVRFIKDHIIVGKD
tne.rse_____ ----MARLFLFDGTALAYRAYYALDRSLSTSTGIPTNATYGVARMLVRFIKDHIIVGKD
ath.rse_____ ----MKLVIFDGNLSILYRAFFALP-ELTTSNNIPTNAIYGfVNVILKYLEQ---EKPD
DPO1_ECOLI    MVQIPQNPLILVDGSSYLRYAHAF-PLTNSAGEPTGAMYGVNLMLRSLIMQ---YKPT
               * . * * . * * * . * . * . * * * * . . . .

chimera_____ YVAVAFDKKAATFRHKLLETYKAQRPKTPDLLIQQLPYIKKLVEALGMKVLEVEGYEADD
tne.rse_____ YVAVAFDKKAATFRHKLLETYKAQRPKTPDLLIQQLPYIKKLVEALGMKVLEVEGYEADD
ath.rse_____ YVAVAFDKRGREARKSEYEYKANRKPMPTNLQVQIPYVREILYAFNIPIIEFEGYEADD
DPO1_ECOLI    HAAVVFDAKGKTFRDELFEHYKSHRPPMPDDLRAQIEPLHAMVKAMGLPLLAVSGVEADD
               * * * * . * * * * * * * * . . . . * * * *

chimera_____ IIATLAVKGLPLFDEIFIVTGDKMLQLVNEKIKVWRIVKGISD--LELYDAQKVKEKYG
chimera_____ IIATLAVKGLPLFDEIFIVTGDKMLQLVNEKIKVWRIVKGISD--LELYDAQKVKEKYG
ath.rse_____ VIGSLVNQFKNTGLDIVIITGDRDTLQLLDKNVVKIVSTKFDKTVEDLYTVENVKEKYG
DPO1_ECOLI    VIGTLAREAEKAGRPVLISTGDKDMAQLVTPNITLINTMTNTILG--PE----EVVNKYG
               . * . * . * * * * * * * . . . . * * * *

chimera_____ VEPQQIPDLLALTGDEIDNIPGVTGIGEKTA VQ LLEKYKDLEDILNHVRELP-----Q
tne.rse_____ VEPQQIPDLLALTGDEIDNIPGVTGIGEKTA VQ LLEKYKDLEDILNHVRELP-----Q
ath.rse_____ VWANQVPDYKALVGDQSDNIPGVKGIGEKSAQKLLEEYSSLEEIYQNLDKIK-----S
DPO1_ECOLI    VPPELIIDFLALMGDSSDNIPGVPGVGEKTAQALLQGLGLDTLYAEPEKIAGLSFRGAK
               * . * * * * * * * * * * * * . . . .

chimera_____ KVRKALLRDRENAILS SKKLAIETNPVPIEINWHEELRYQGYDREKLLPLLKELEFASIMKE
tne.rse_____ KVRKALLRDRENAILS SKKLAIETNPVPIEINWHEELRYQGYDREKLLPLLKELEFASIMKE
ath.rse_____ SIREKLEAGKDMAFLSKRLATIVCDLPLNVKLEDLRTKEWNKERLYEILVQLEFKSIIKR
DPO1_ECOLI    TMAAKLEQNKEVAYLSYQLATIKTDVELELTCEQLEVQQPAAEELLGLFKKYEFKRWTAD
               . * . . * * * * * * . . . . * * . * * . * *

chimera_____ LQLYEESEPVGYRIVK-----DIVEFEKLEIEKLRESP
tne.rse_____ LQLYEESEPVGYRIVK-----DIVEFEKLEIEKLRESP
ath.rse_____ LGLS-----EVVQFEFVQQRDIPD
DPO1-ECOLI    VEAGKWLQAKGAKPAAKPQETSVADEAPEVTATVISYDNYVTILDEETLKAWIAKLEKAP
               .

chimera_____ SFAIDLETSSLDPFDCDIVGISVSFKPKAEAYYIPLHHRNAQNLDKE---VLKKLKEILE
tne.rse_____ SFAIDLETSSLDPFDCDIVGISVSFKPKAEAYYIPLHHRNAQNLDKE---VLKKLKEILE
ath.rse_____ VEQKELESISQIRSKE--IPLMFVQGEK-CFYLYDQESNTVFITSN-----KLLIEEIL
DPO1_ECOLI    VFAFDTETDSLNDNISANLVGLSFAIEPGVAAYIPVAHDYLDAPDQISRERALELLKPLLE
               . * . * . . . * . . .

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chimera____
tne.rse____
ath.rse____
DPO1_ECOLI

DPGAKIVGQNLKFDYKVLVVGVEPVPPHFDTMIAAYLLEPNEKKFNLDLALKFLGYKM
DPGAKIVGQNLKFDYKVLVVGVEPVPPHFDTMIAAYLLEPNEKKFNLDLALKFLGYKM
KSDTVKIMYDLKNI FHQLNLEDTNNIKNCEDVMIASYVLDSTRSSYELETFLVSYLNTDI
DEKALKVGVNLKYDRGILANYGIELRGIAFDTMLESYILNSVAGRHDMSLAERWLKHKT
* * * * *

chimera____
tne.rse____
ath.rse____
DPO1_ECOLI

TSYQELMSFSSPLFGFSFADVPVEKAANYSCEDADITYRLYKILSLKLHEAD-LENVFYK
TSYQELMSFSSPLFGFSFADVPVEKAANYSCEDADITYRLYKILSLKLHEAD-LENVFYK
EAVKKDKKIVS-----VLLKRLWDELLRLIDLNS-CQFLYEN
ITFEEIAGKGKNQ--LTFNQIALEEAGRYAAEDADVTQLHLKMWPDQLQKHGKPLNVFEN
* * * * *

chimera____
tne.rse____
ath.rse____
DPO1-ECOLI

IEMPLVSVLARMELNGVKVDRDALIQYTKEIENKILKLETQIYQIAGEWFNINSPKQLSY
IEMPLVSVLARMELNGVYVDTEFLKKLSEEGYKKEELAEIYRIAGEPNINSPKQVSR
IERPLIPVLYEMEKTFGKVDRLDALIQYTKEIENKILKLETQIYQIAGEWFNINSPKQLSY
IEMPLVPVLSRIERNVGKIDPKVLHNSSEELTLRLAELEKKAHEIAGEEFNLSSTKQLQT
* * * * *

chimera____
tne.rse____
ath.rse____
DPO1_ECOLI

ILFEKLKLPVIKKTGTG--YSTDAEVLEELFDKHEIVPLILDYRMYTKILTYYCQGLLQA
ILFEKLGIKPRGKTTKTGDYSTRIEVLEELAGEHEIIPILILEYRKIQKLKSTYIDALPKM
ILFEKLKLPVIKKTGTG--YSTDAEVLEELFDKHEIVPLILDYRMYTKILTYYCQGLLQA
ILFEKQGIKPLKKTGG-APSTSEEVLEELALDYPLPKVILEYRGLAKLKSTYTDKPLPM
* * * * *

chimera____
tne.rse____
ath.rse____
DPO1-ECOLI

INPSSGRVHTTFIQTGTATGRLESSDPNLQNI PVKYDEGKLIRKVFVPEG-GHVLIDADY
VNPKTGRIHASFNQTGTATGRLESSDPNLQNLPTKSEEGKEIRKAIVPQDPNWWIVSADY
INPSSGRVHTTFIQTGTATGRLESSDPNLQNI PVKYDEGKLIRKVFVPEG-GHVLIDADY
INPKTGRVHTSYHQA VTATGRLSSTDPNLQNI PVRNEEGRRIRQAFIAPE-DYVIVSADY
* * * * *

chimera____
tne.rse____
ath.rse____
DPO1_ECOLI

SQIELRILAHISEDRLISAFKNNVDIHSQTAAEVFGVDIADVTPEMRSQAKAVNFGIVY
SQIELRILAHLSGDNLLRAFEEGIDVHTLTASRIFNVKPEEVTEEMRRAGKMNFSIIY
SQIELRILAHISEDRLISAFKNNVDIHSQTAAEVFGVDIADVTPEMRSQAKAVNFGIVY
SQIELRIMAHLSRDKGLLTAFAGKDIHRATAAEVFGVPLET VTSEQRSAKAINFGLIY
* * * * *

chimera____
tne.rse____
ath.rse____
DPO1_ECOLI

GISDYGLARDIKISRKEAAEFINKY FERYPKVKEYLDNTV KFARDNGFVLTFLNRKRYIK
GVTPYGLSVRLGVPVKEAEKMIVNYFVLYPKVRDYIQRVVSEAKEKGYVRTLFGRKRDIP
GISDYGLARDIKISRKEAAEFINKY FERYPKVKEYLDNTV KFARDNGFVLTFLNRKRYIK
GMSAFGLARQLNIPRKEAQKYMDLY FERYPGVLEYMERTRAQAKEQGYVETLDGRRLYLP
* * * * *

chimera____
tne.rse____
ath.rse____
DPO1_ECOLI

DIKSTNRNLRGYAERIA MNSPIQGSAADIMKLAMIKVYQKLKENNLKSKII LQVHDELLI
QLMARDRNTQAEGERIAINTPIQGTAA DI IKLAMIEIDRELKERKMRSKMII QVHDELVF
DIKSTNRNLRGYAERIA MNSPIQGSAADIMKLAMIKVYQKLKENNLKSKII LQVHDELLI
DIKSSNGARRAAAERA AINAPMQGTAA DI IKRAMIAVDWLQAEQPRVRMIMQVHDELVF
* * * * *

Fig. 17/3

chimera_____
tne.rse_____
ath.rse_____
DPO1_ECOLI

EAPYEEKDIVKEIVKREMANAVALKVPLVVEVKEGLNWEYENKI
EVPNEEKDALVELVKDRMTNVVKLSVPLEVDVTIGKTWS----
EAPYEEKDIVKEIVKREMANAVALKVPLVVEVKEGLNWEYENKI
EVHKDDVDAAKQIHQLMENCTRLDVPLLVEVGSGENWDQAH-
* .. * . . . * * * * * * * * *

Figure 18/1:

SEQ ID No.: 19

SEQ ID No.: 20

SEQ ID No.: 21

SEQ ID NO.: 22

TNE UP 5' CTG ACC ATG GCG AGA CTA TTT CTC TTT G -3'
 TNE LOW 5' TCT GTC GAC CTT CAC ACC GTT CAG TTC CAT CC -3'
 ATH UP 5' - AAG GTC GAC AGA GAT GCC CTC ATC CAA TAT ACC -3'
 ATH LOW 5' - TAG CAA GCT TCT ATT TTG TCT CAT ACC AGT -3'

A.

crossing point 1

SEQ ID No.: 23

SEQ ID No.: 24

SEQ ID No.: 25

chimera__8 IEMPLVSVLARMELNGV | KVDRDALIQYTKIEIENKILKLETQIYQIAGEWFNINSPKQLSY
 tne.rse__ IEMPLVSVLARMELNGV | YVDTEFLKKLSEYGGKLEELAEIYRIAGEPFNINSPKQVSR
 ath.rse__ IERPLIPVLYEMEKTGF | KVDRDALIQYTKIEIENKILKLETQIYQIAGEWFNINSPKQLSY

B.

SEQ ID No.: 19

SEQ ID No.: 26

SEQ ID No.: 27

5' ctg acc ATG GCG AGA CTA TTT CTC TTT G -3'
 TNEUP |----->
 ATG GCG AGA CTA TTT CTC TTT GAT GGA 27
 M A R L F L F D G 9

1

SEQ ID No.: 28

SEQ ID No.: 29

SEQ ID No.: 20

SEQ ID No.: 21

SEQ ID No.: 30

SEQ ID No.: 31

1512 CGG ATG GAA CTG AAC GGT GTG TAC GTG GAC ACA GAG TTC CTG AAG AAA CTC 1563
 505 R M E L N G V Y V D T E F L K K L 521
 3'CC CAT CTT GAC TTG CCA CAC ctt Cag cTG TcT 5'

<-----=====| TNELOW

"Sal I site "

ATHUP |----->
 5' AAG Gtc Gac AGA GAT GCC CTC ATC CAA TAT ACC -3'
 1387 ATG GAA AAA ACA GGA TTT AAG GTG GAT AGA GAT GCC CTC ATC CAA TAT ACC 1435
 463 M E K T G F K V D R D A L I Q Y T 479

Figure 18/2:

SEQ ID No.: 32

SEQ ID No.: 33

SEQ ID No.: 22

```
2526   GGA CTG AAC TGG TAT GAG ACA AAA TAG           2553
843    G  L  N  W  Y  E  T  K  *
      3' TG ACC ATA CTC TGT TTT ATC ttcgaacgat 5'
      <-----| ATHLOW
```

Figure 19:

SEQ ID No.: 34

SEQ ID No.: 35

SEQ ID No.: 36

crossing point 2

```

chimera__8  IMEPLVSVLARMELNGVYVDTEFLKKLSEELYGKKLEELAEIYRIAGEPFNINSPKQVS|R
tne.rse_____IEMPLVSVLARMELNGVYVDTEFLKKLSEELYGKKLEELAEIYRIAGEPFNINSPKQVS|R
ath.rse_____IERPLIPVLYEMEKTGFKVDRDALIQYTKIENKILKLETQIYQIAGEWFNINSPKQLS|R

```

A.

TNE polymerase nucleotide sequence 1642-1689

SEQ ID No.: 37

SEQ ID No.: 38

Bam HI site

```

=====
1642  TCA CCG AAG CAG GTT TCA AGG ATC CTT TTT GAA AAA CTC GGC ATA AAA 1689
548   S  P  K  Q  V  S  R  I  L  F  E  K  L  G  I  K  563

```

SEQ ID No.: 39

SEQ ID No.: 40

SEQ ID No.: 41

SEQ ID No.: 42

ATH polymerase nucleotide sequence 1513 - 1560

```

1513  TCA CCG AAA CAG CTT TCT TAC ATT TTG TTT GAA AAG CTA AAA CTT CCT 1560
505   S  P  K  Q  L  S  Y  I  L  F  E  K  L  K  L  P  520

```

```

5'CA CCG AAA CAG CTT TCT agg atc cTG TTT GAA AAG CTA AAA CTT CCT G 3'
|-----m1----->

```

```

.....3'GT GGC TTT GTC GAA AGA tcc tag gAC AAA CTT TTC GAT TTT GAA GGA C 5'
<-----m2-----|

```

B.

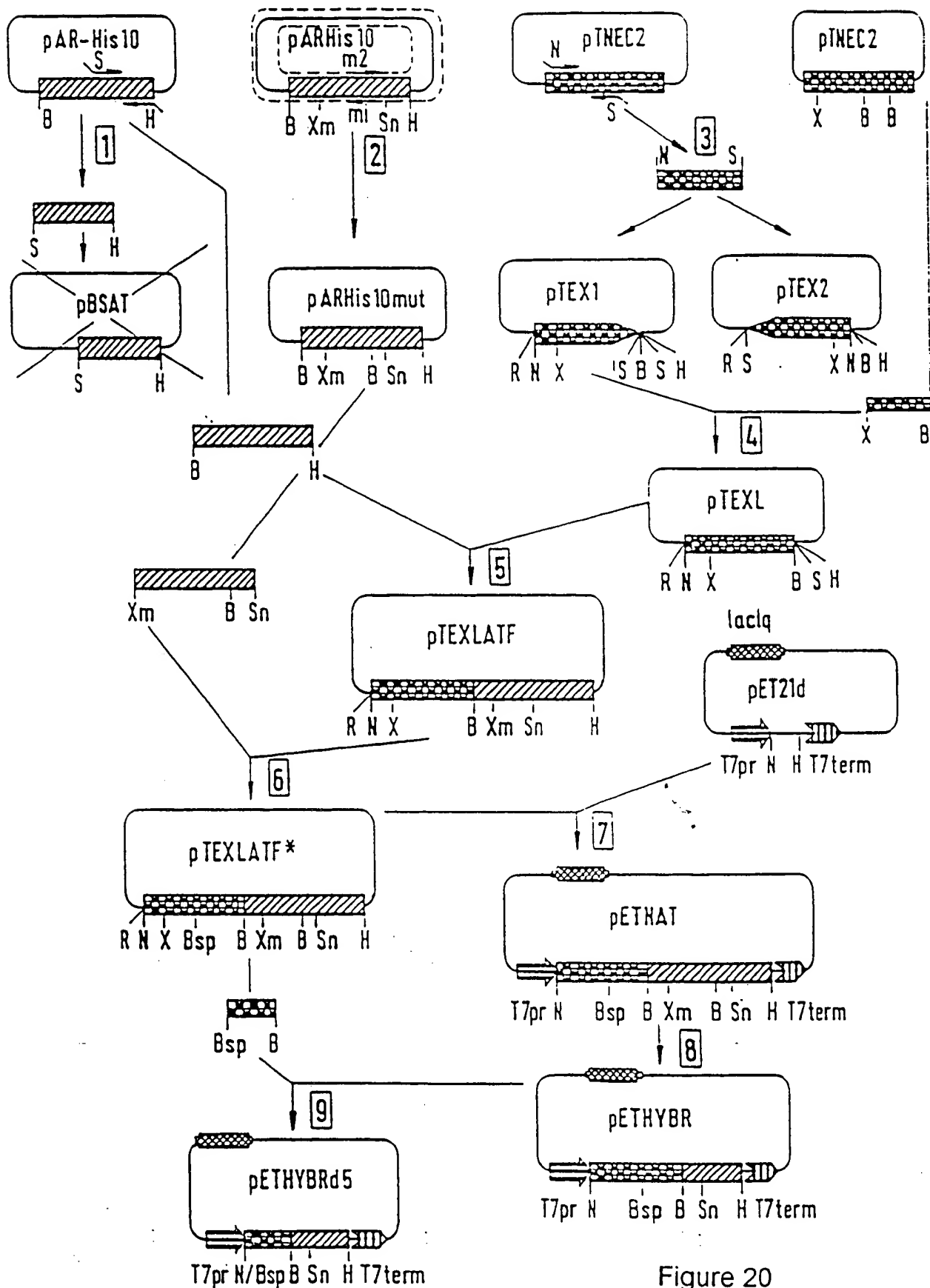


Figure 20

Figure 21:

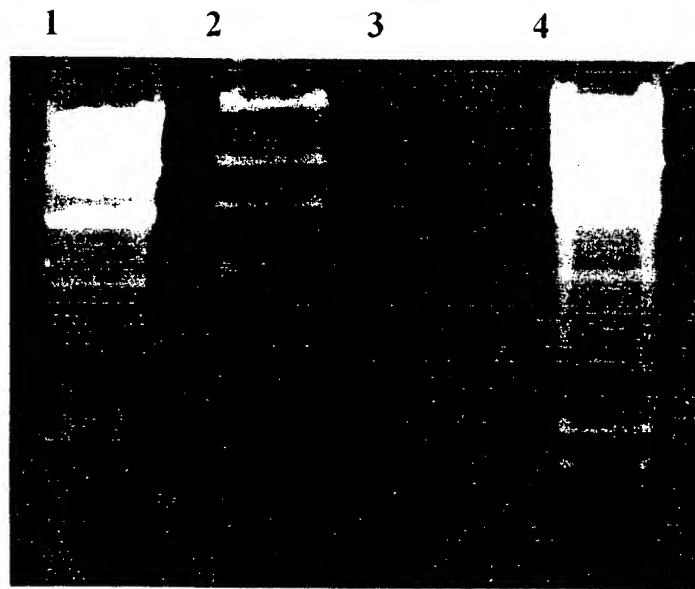


Figure 22:

Comparison of the reverse transcriptase activity of
Tne/Ath hybrid polymerases with Tth- and C.therm.
polymerase

